

## AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

### LISTING OF CLAIMS:

Claim 1 (Cancelled)

2. (Original) An isolated negative-sense single stranded RNA virus (MPV) belonging to the sub-family *Pneumovirinae* of the family *Paramyxoviridae* and identifiable as phylogenetically corresponding to the genus *Metapneumovirus* by determining a nucleic acid sequence of said virus and testing it in phylogenetic tree analyses wherein maximum likelihood trees are generated using 100 bootstraps and 3 jumbles and finding it to be more closely phylogenetically corresponding to a virus isolate deposited as **I-2614** with CNCM, Paris than it is corresponding to a virus isolate of avian pneumovirus (APV) also known as turkey rhinotracheitis virus (TRTV), the aetiological agent of avian rhinotracheitis.

Claims 3 to 58 (Cancelled)

59. (Currently amended) A method for detecting a human metapneumovirus in a sample. ~~The method of claim 48, 49, 50 or 51,~~ wherein the method further comprises contacting the sample with a nucleic acid encoding an amino acid sequence that is:

- (a) an amino acid sequence that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1 or 99-1 as shown in Figure 20;
- (b) an amino acid sequence that is greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 or 99-1 as shown in Figure 21;
- (c) an amino acid sequence that is greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 or 99-1 as shown in Figure 22;
- (d) an amino acid sequence that is greater than 81% identical to the amino acid sequence of the F protein of MPV isolate 00-1 or 99-1 as shown in Figure 23;
- (e) an amino acid sequence that is greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 or 99-1 as shown in Figure 24;

- (f) an amino acid sequence that is greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 or 99-1 as shown in Figure 25;
- (g) an amino acid sequence that is greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 or 99-1 as shown in Figure 28;
- (h) an amino acid sequence that is greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 or 99-1 as shown in Figure 26; or
- (i) an amino acid sequence that is greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 or 99-1 as shown in Figure 27.

60. (Currently amended) A method for detecting a human metapneumovirus in a sample, The method of claim 48, 49, 50 or 51, wherein the method ~~further~~ comprises contacting the sample with an antibody that specifically binds to a protein that is:

- (a) greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1 or 99-1 as shown in Figure 20;
- (b) greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 or 99-1 as shown in Figure 21;
- (c) greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 or 99-1 as shown in Figure 22;
- (d) greater than 81 % identical to the amino acid sequence of the F protein of MPV isolate 00-1 or 99-1 as shown in Figure 23;
- (e) greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 or 99-1 as shown in Figure 24;
- (f) greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 or 99-1 as shown in Figure 25;
- (g) greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 or 99-1 as shown in Figure 28;
- (h) greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 or 99-1 as shown in Figure 26; or
- (i) greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 or 99-1 as shown in Figure 27.

61. (Currently amended) A method for detecting a human metapneumovirus in a sample, The method of claim 48, 49, 50 or 51, wherein the method ~~further~~ comprises

contacting the sample with a first group of one or more nucleic acids that hybridize under stringent conditions to a second group of one or more nucleic acids, that encodes a protein, or fragment thereof, comprising,

- (a) a sequence that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1 and 99-1 as shown in figure 20;
  - (b) a sequence that is greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 and 99-1 as shown in figure 21;
  - (c) a sequence that is greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 and 99-1 as shown in figure 22;
  - (d) a sequence that is greater than 81% identical to the amino acid sequence of the F protein of MPV isolate 00-1 and 99-1 as shown in figure 23;
  - (e) a sequence that is greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 and 99-1 as shown in figure 24;
  - (f) a sequence that is greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 and 99-1 as shown in figure 25;
  - (g) a sequence that is greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 and 99-1 as shown in figure 28;
  - (h) a sequence that is greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 and 99-1 as shown in figure 26; or
  - (i) a sequence that is greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 and 99-1 as shown in figure 27,
- wherein sequence identity is determined over the entire length of the protein.

62. (Currently amended) A method for detecting a human metapneumovirus in a sample. ~~The method of claim 48, 49, 50 or 51,~~ wherein the method ~~further~~ comprises contacting the sample with one or more nucleic acids that hybridize under stringent conditions to the genome or antigenome of the virus isolate deposited as I-2614 with CNCM, Paris.

63. (New) The method of claim 59, wherein the amino acid is:
- (i) SEQ ID No.: 64 or 98;
  - (ii) SEQ ID No.: 21 or 94;
  - (iii) SEQ ID No.: 99 or 100;
  - (iv) SEQ ID No.: 47 or 95;

- (v) SEQ ID No.: 55 or 96;
- (vi) SEQ ID No.: 14 or 93;
- (vii) SEQ ID No.: 1 or 91;
- (viii) SEQ ID No.: 8 or 92; or
- (ix) SEQ ID No.: 63 or 97.

64. (New) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with a primer selected from the group consisting of SEQ ID No.: 113-120.

65. (New) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with a probe having the nucleic acid sequence of SEQ ID No.: 121, 122 or 123.

66. (New) The method of claim 60, wherein the protein consists of an amino acid sequence of:

- (i) SEQ ID No.: 64 or 98;
- (ii) SEQ ID No.: 21 or 94;
- (iii) SEQ ID No.: 99 or 100;
- (iv) SEQ ID No.: 47 or 95;
- (v) SEQ ID No.: 55 or 96;
- (vi) SEQ ID No.: 14 or 93;
- (vii) SEQ ID No.: 1 or 91;
- (viii) SEQ ID No.: 8 or 92; or
- (ix) SEQ ID No.: 63 or 97.

67. (New) The method of claim 66, wherein the method further comprises an immune fluorescence assay.

68. (New) A method for detecting an antibody against human metapneumovirus in a sample, wherein the method comprises contacting the sample with a protein comprising the amino acid sequence of:

- (i) SEQ ID No.: 64 or 98;
- (ii) SEQ ID No.: 21 or 94;

- (iii) SEQ ID No.: 99 or 100;
- (iv) SEQ ID No.: 47 or 95;
- (v) SEQ ID No.: 55 or 96;
- (vi) SEQ ID No.: 14 or 93;
- (vii) SEQ ID No.: 1 or 91;
- (viii) SEQ ID No.: 8 or 92; or
- (ix) SEQ ID No.: 63 or 97.